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## SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research  
Organisation AND  
5 Australian Wool Research and Promotion Organisation

<120> Method of modifying plant productivity

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<140> PCT/AU00/XXXXX  
<141> 2000-09-23

<150> AU PQ3049  
15 <151> 1999-09-24

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<170> PatentIn Ver. 2.0  
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Tyr Ala Pro Phe Phe Ser Leu Ala Asn Lys Ser Ala Ile Ser Pro Asp  
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	Ser Ser Arg Val Ile Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe Gln	145	150	155	160
	agc acc aag ctg aag gat cct cgt gcc cag ccc ggc caa tcg tcg ccc				528
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PCT/AU00/01183

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PCT/AU00/01183

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	ggc gca ggt aac ccg ctc ggc ccg acc cag ggc gtc ggc tac gct aac			1008
	Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn			
		325	330	335
	gag ctc atc gcc cgt ctc acc cac tcg cct gtc cac gat gac acc agc			1056
	Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr Ser			
		340	345	350
	tcc aac cac aca ttg gac tcc aac ccg gct act ttc ccg ctc aac tcc			1104
40	Ser Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ser			
		355	360	365

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act ctc tat gcg gac ttt tcg cat gat aac ggc atc atc tct atc ctc 1152  
 Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile Leu  
 370 375 380

5 ttt gct ttg ggt ctg tac aac ggc acc aag ccg ctg tct tcc acg acc 1200  
 Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Ser Thr Thr  
 385 390 395 400

10 gcg gag aat atc acc cag acc gat ggg ttc tca tct gcc tgg acg gtt 1248  
 Ala Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr Val  
 405 410 415

cct ttc gcg tcg cgc atg tac gtc gag atg atg caa tgc cag tcc gag 1296  
 Pro Phe Ala Ser Arg Met Tyr Val Glu Met Met Gln Cys Gln Ser Glu  
 15 420 425 430

cag gag cct ttg gtc cgt gtc ttg gtt aat gat cgt gtt gtt ccg ctg 1344  
 Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu  
 435 440 445

20 cat ggc tgt ccg gtt gat gct ttg gga aga tgt acg cgg gat agc ttc 1392  
 His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe  
 450 455 460

25 gtg aag ggg ttg agc ttt gcc aga tct ggc ggt gat tgg gcg gag tgt 1440  
 Val Lys Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys  
 465 470 475 480

30 ttt gct tag 1449  
 Phe Ala

<210> 10  
 <211> 482  
 35 <212> PRT  
 <213> Artificial Sequence

<400> 10  
 Met Gly Arg Ile Ala Arg Gly Ser Lys Met Ser Ser Leu Ile Val Ser  
 40 1 5 10 15  
 Leu Leu Val Val Leu Val Ser Leu Asn Leu Ala Ser Glu Thr Thr Ala



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	20	25	30
	Ala Met Leu Ala Val Pro Ala Ser Arg Asn Gln Ser Thr Cys Asp Thr		
	35	40	45
5	Val Asp Gln Gly Tyr Gln Cys Phe Ser Glu Thr Ser His Leu Trp Gly		
	50	55	60
	Gln Tyr Ala Pro Phe Phe Ser Leu Ala Asn Lys Ser Ala Ile Ser Pro		
10	65	70	75 80
	Asp Val Pro Ala Gly Cys His Val Thr Phe Ala Gln Val Leu Ser Arg		
	85	90	95
15	His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala		
	100	105	110
	Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr Thr Phe Glu Gly Lys Tyr		
	115	120	125
20	Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr		
	130	135	140
	Pro Phe Gly Glu Gln Glu Leu Val Asn Ser Gly Val Lys Phe Tyr Gln		
25	145	150	155 160
	Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val Pro Phe Ile Arg Ser Ser		
	165	170	175
30	Gly Ser Asn Arg Val Ile Ala Ser Gly Asn Lys Phe Ile Glu Gly Phe		
	180	185	190
	Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser		
	195	200	205
35	Pro Lys Ile Asp Val Val Ile Ser Glu Ala Ser Thr Ser Asn Asn Thr		
	210	215	220
	Leu Asp Pro Gly Thr Cys Thr Val Phe Glu Asp Ser Glu Leu Ala Asp		
40	225	230	235 240
	Asp Ile Glu Ala Asn Phe Thr Ala Thr Phe Val Pro Ser Ile Arg Gln		

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	245	250	255
	Arg Leu Glu Asn Asp Leu Ser Gly Val Ser Leu Thr Asp Thr Glu Val		
	260	265	270
5	Thr Tyr Leu Met Asp Met Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr		
	275	280	285
	Val Asp Thr Lys Leu Ser Pro Phe Cys Asp Leu Phe Thr His Glu Glu		
10	290	295	300
	Trp Ile Asn Tyr Asp Tyr Leu Gln Ser Pro Asn Lys Tyr Tyr Gly His		
	305	310	315 320
15	Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn		
	325	330	335
	Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr Ser		
	340	345	350
20	Ser Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ser		
	355	360	365
	Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile Leu		
25	370	375	380
	Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Ser Thr Thr		
	385	390	395 400
30	Ala Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr Val		
	405	410	415
	Pro Phe Ala Ser Arg Met Tyr Val Glu Met Met Gln Cys Gln Ser Glu		
	420	425	430
35	Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu		
	435	440	445
	His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe		
40	450	455	460
	Val Lys Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys		

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465
470
475
480

Phe Ala

5

<210> 11
<211> 1449
<212> DNA
10 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:chimeric
      ext::phyA-l gene

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<220>
<221> CDS
<222> (1)..(1446)

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    atg gga aga att gct aga ggc tca aaa atg agt tct ctc att gtg tct    48
    Met Gly Arg Ile Ala Arg Gly Ser Lys Met Ser Ser Leu Ile Val Ser
      1             5             10             15

25    ttg ctt gta gta ttg gtg tca ctc aat ttg gct tcc gaa acc aca gct    96
    Leu Leu Val Val Leu Val Ser Leu Asn Leu Ala Ser Glu Thr Thr Ala
      20             25             30

    gcc atg ctg gca gtc ccc gcc tcg aga aat caa tcc agt tgc gat acg    144
    Ala Met Leu Ala Val Pro Ala Ser Arg Asn Gln Ser Ser Cys Asp Thr
      35             40             45

    gtc gat cag ggg tat caa tgc ttc tcc gag act tcg cat ctt tgg ggt    192
    Val Asp Gln Gly Tyr Gln Cys Phe Ser Glu Thr Ser His Leu Trp Gly
      50             55             60

35    caa tac gca ccg ttc ttc tct ctg gca aac gaa tcg gtc atc tcc cct    240
    Gln Tyr Ala Pro Phe Phe Ser Leu Ala Asn Glu Ser Val Ile Ser Pro
      65             70             75             80

40    gag gtg ccc gcc gga tgc aga gtc act ttc gct cag gtc ctc tcc cgt    288
    Glu Val Pro Ala Gly Cys Arg Val Thr Phe Ala Gln Val Leu Ser Arg

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	85	90	95	
	cat gga gcg cgg tat ccg acc gac tcc aag ggc aag aaa tac tcc gct			336
	His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala			
5	100	105	110	
	ctc att gag gag atc cag cag aac gcg acc acc ttt gac gga aaa tat			384
	Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr Thr Phe Asp Gly Lys Tyr			
	115	120	125	
10				
	gcc ttc ctg aag aca tac aac tac agc ttg ggt gca gat gac ctg act			432
	Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr			
	130	135	140	
15				
	ccc ttc gga gaa cag gag cta gtc aac tcc ggc atc aag ttc tac cag			480
	Pro Phe Gly Glu Gln Glu Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln			
	145	150	155	160
	cgg tac gaa tcg ctc aca agg aac atc gtt cca ttc atc cga tcc tct			528
20	Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val Pro Phe Ile Arg Ser Ser			
	165	170	175	
	ggc tcc agc cgc gtg atc gcc tcc ggc aag aaa ttc atc gag ggc ttc			576
	Gly Ser Ser Arg Val Ile Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe			
25	180	185	190	
	cag agc acc aag ctg aag gat cct cgt gcc cag ccc ggc caa tcg tcg			624
	Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser			
	195	200	205	
30				
	ccc aag atc gac gtg gtc att tcc gag gcc agc tca tcc aac aac act			672
	Pro Lys Ile Asp Val Val Ile Ser Glu Ala Ser Ser Ser Asn Asn Thr			
	210	215	220	
	ctc gac cca ggc acc tgc act gtc ttc gaa gac agc gaa ttg gcc gat			720
	Leu Asp Pro Gly Thr Cys Thr Val Phe Glu Asp Ser Glu Leu Ala Asp			
	225	230	235	240
35				
	acc gtc gaa gcc aat ttc acc gcc acg ttc gtc ccc tcc att cgt caa			768
40	Thr Val Glu Ala Asn Phe Thr Ala Thr Phe Val Pro Ser Ile Arg Gln			
	245	250	255	

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	cgt ctg gag aac gac ctg tcc ggt gtg act ctc aca gac aca gaa gtg	816
	Arg Leu Glu Asn Asp Leu Ser Gly Val Thr Leu Thr Asp Thr Glu Val	
	260 265 270	
5	acc tac ctc atg gac atg tgc tcc ttc gac acc atc tcc acc agc acc	864
	Thr Tyr Leu Met Asp Met Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr	
	275 280 285	
10	gtc gac acc aag ctg tcc ccc ttc tgt gac ctg ttc acc cat gac gaa	912
	Val Asp Thr Lys Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp Glu	
	290 295 300	
15	tgg atc aac tac gac tac ctc cag tcc ttg aaa aag tat tac ggc cat	960
	Trp Ile Asn Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly His	
	305 310 315 320	
20	ggt gca ggt aac ccg ctc ggc ccg acc cag ggc gtc ggc tac gct aac	1008
	Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn	
	325 330 335	
	gag ctc atc gcc cgt ctg acc cac tcg cct gtc cac gat gac acc agt	1056
	Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr Ser	
	340 345 350	
25	tcc aac cac act ttg gac tcg agc ccg gct acc ttt ccg ctc aac tct	1104
	Ser Asn His Thr Leu Asp Ser Ser Pro Ala Thr Phe Pro Leu Asn Ser	
	355 360 365	
30	act ctc tac gcg gac ttt tcg cat gac aac ggc atc atc tcc att ctc	1152
	Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile Leu	
	370 375 380	
35	ttt gct tta ggt ctg tac aac ggc act aag ccg cta tct acc acg acc	1200
	Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr Thr	
	385 390 395 400	
40	gtg gag aat atc acc cag aca gat gga ttc tcg tct gct tgg acg gtt	1248
	Val Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr Val	
	405 410 415	
	ccg ttt gct tcg cgt ttg tac gtc gag atg atg cag tgt cag gcg gag	1296
	Pro Phe Ala Ser Arg Leu Tyr Val Glu Met Met Gln Cys Gln Ala Glu	

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	420	425	430	
	cag gag ccg ctg gtc cgt gtc ttg gtt aat gat cgc gtt gtc ccg ctg			1344
	Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu			
5	435	440	445	
	cat ggg tgt ccg gtt gat gct ttg ggg aga tgt acc cgg gat agc ttt			1392
	His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe			
	450	455	460	
10				
	gtg agg ggg ttg agc ttt gct aga tct ggg ggt gat tgg gcg gag tgt			1440
	Val Arg Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys			
	465	470	475	480
15	ttt gct tag			1449
	Phe Ala			
20	<210> 12			
	<211> 482			
	<212> PRT			
	<213> Artificial Sequence			
25	<400> 12			
	Met Gly Arg Ile Ala Arg Gly Ser Lys Met Ser Ser Leu Ile Val Ser			
	1 5 10 15			
	Leu Leu Val Val Leu Val Ser Leu Asn Leu Ala Ser Glu Thr Thr Ala			
	20 25 30			
30				
	Ala Met Leu Ala Val Pro Ala Ser Arg Asn Gln Ser Ser Cys Asp Thr			
	35 40 45			
35	Val Asp Gln Gly Tyr Gln Cys Phe Ser Glu Thr Ser His Leu Trp Gly			
	50 55 60			
	Gln Tyr Ala Pro Phe Phe Ser Leu Ala Asn Glu Ser Val Ile Ser Pro			
	65 70 75 80			
40	Glu Val Pro Ala Gly Cys Arg Val Thr Phe Ala Gln Val Leu Ser Arg			
	85 90 95			

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	His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala	
	100	105 110
5	Leu Ile Glu Glu Ile Gln Gln Asn Ala Thr Thr Phe Asp Gly Lys Tyr	
	115	120 125
	Ala Phe Leu Lys Thr Tyr Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr	
	130	135 140
10	Pro Phe Gly Glu Gln Glu Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln	
	145	150 155 160
	Arg Tyr Glu Ser Leu Thr Arg Asn Ile Val Pro Phe Ile Arg Ser Ser	
	165	170 175
15	Gly Ser Ser Arg Val Ile Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe	
	180	185 190
	Gln Ser Thr Lys Leu Lys Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser	
20	195	200 205
	Pro Lys Ile Asp Val Val Ile Ser Glu Ala Ser Ser Ser Asn Asn Thr	
	210	215 220
25	Leu Asp Pro Gly Thr Cys Thr Val Phe Glu Asp Ser Glu Leu Ala Asp	
	225	230 235 240
	Thr Val Glu Ala Asn Phe Thr Ala Thr Phe Val Pro Ser Ile Arg Gln	
	245	250 255
30	Arg Leu Glu Asn Asp Leu Ser Gly Val Thr Leu Thr Asp Thr Glu Val	
	260	265 270
	Thr Tyr Leu Met Asp Met Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr	
35	275	280 285
	Val Asp Thr Lys Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp Glu	
	290	295 300
40	Trp Ile Asn Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly His	
	305	310 315 320

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Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn  
 - 325 330 335

5 Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val His Asp Asp Thr Ser  
 340 345 350

Ser Asn His Thr Leu Asp Ser Ser Pro Ala Thr Phe Pro Leu Asn Ser  
 355 360 365

10 Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile Leu  
 370 375 380

Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr Thr  
 385 390 395 400

15 Val Glu Asn Ile Thr Gln Thr Asp Gly Phe Ser Ser Ala Trp Thr Val  
 405 410 415

Pro Phe Ala Ser Arg Leu Tyr Val Glu Met Met Gln Cys Gln Ala Glu  
 20 420 425 430

Gln Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu  
 435 440 445

25 His Gly Cys Pro Val Asp Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe  
 450 455 460

Val Arg Gly Leu Ser Phe Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys  
 30 465 470 475 480

Phe Ala

35 <210> 13  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

40 <220>  
 <223> Description of Artificial Sequence:primer



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<400> 13  
cgcggaattca tgctggcagt ccccgccctcg 30

5 <210> 14  
<211> 27  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Description of Artificial Sequence:primer

<400> 14  
ggcatcgatc taagcaaaac actccgc 27

15

<210> 15  
<211> 32  
<212> DNA

20 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

25 <400> 15  
gcgtctagag aattcatggg aagaattgct ag 32

<210> 16

30 <211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

35

<400> 16  
cgcggatccg cggccgcagc tgtggtttcg gaagc 35

40

<210> 17  
<211> 17

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<212> DNA  
<213> Artificial Sequence

<220>  
5 <223> Description of Artificial Sequence:ext::phytase  
junction

<400> 17  
10 acgctgccat gctggca 17

<210> 18  
<211> 6  
<212> PRT  
15 <213> Artificial Sequence

<220>  
20 <223> Description of Artificial Sequence:ext::phytase  
junction

<400> 18  
Thr Ala Ala Met Leu Ala  
1 5

25